



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 04:05 am BST

PDB ID : 4NO6
Title : yCP in complex with Z-Leu-Leu-Leu-vinylsulfone
Authors : Stein, M.L.; Cui, H.; Beck, P.; Dubiella, C.; Voss, C.; Krueger, A.; Schmidt, B.; Groll, M.
Deposited on : 2013-11-19
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

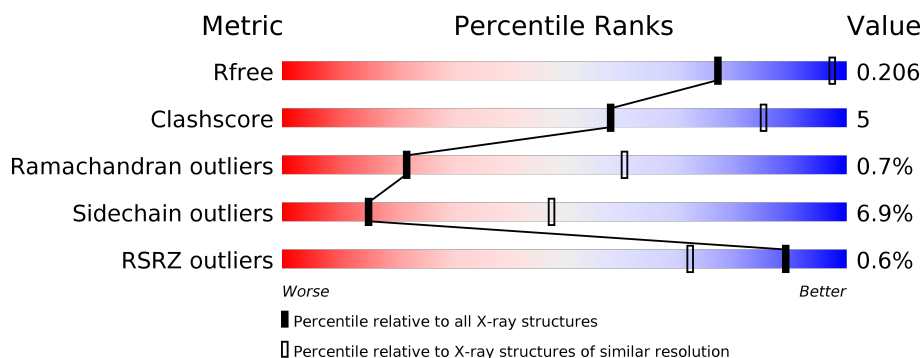
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.














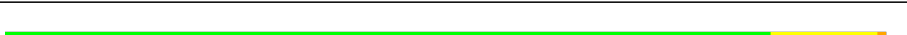


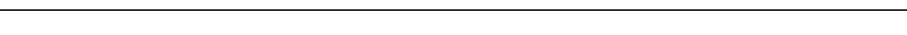
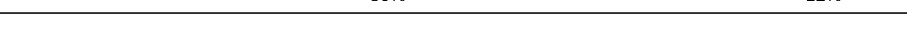

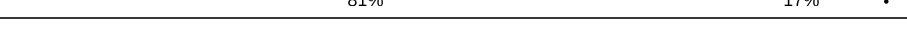

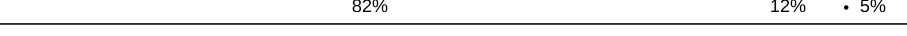


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	<div> <div>90%</div> <div>9%</div> <div>•</div> </div>
1	O	250	<div> <div>87%</div> <div>12%</div> <div>•</div> </div>
2	B	258	<div> <div>2%</div> <div>73%</div> <div>17%</div> <div>• • 5%</div> </div>
2	P	258	<div> <div>3%</div> <div>73%</div> <div>19%</div> <div>• 5%</div> </div>
3	C	254	<div> <div>2%</div> <div>77%</div> <div>15%</div> <div>• 6%</div> </div>
3	Q	254	<div> <div>3%</div> <div>78%</div> <div>13%</div> <div>• 6%</div> </div>

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Mol	Chain	Length	Quality of chain
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49661 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

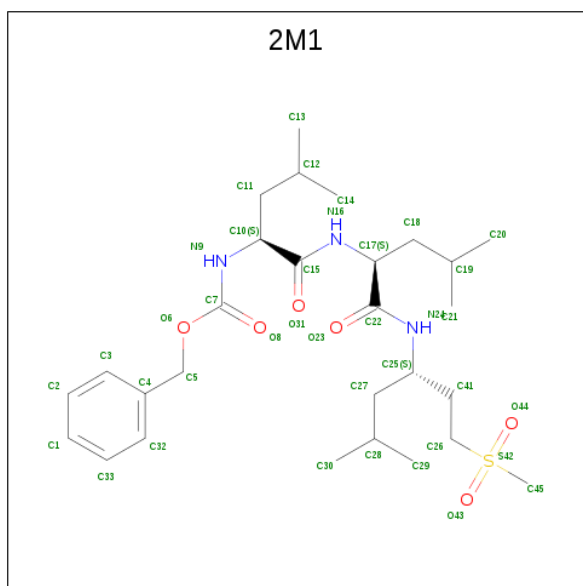
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	1	Total	Mg	0	0
			1	1		
15	I	1	Total	Mg	0	0
			1	1		
15	V	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		
15	N	1	Total	Mg	0	0
			1	1		
15	Y	1	Total	Mg	0	0
			1	1		

- Molecule 16 is N-[(benzyloxy)carbonyl]-L-leucyl-N-[(3S)-5-methyl-1-(methylsulfonyl)hexan-3-yl]-L-leucinamide (three-letter code: 2M1) (formula: C₂₈H₄₇N₃O₆S).



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	B	8	Total O 8 8	0	0
17	C	4	Total O 4 4	0	0
17	D	11	Total O 11 11	0	0
17	E	5	Total O 5 5	0	0
17	F	11	Total O 11 11	0	0
17	G	11	Total O 11 11	0	0
17	H	14	Total O 14 14	0	0
17	I	7	Total O 7 7	0	0
17	J	11	Total O 11 11	0	0
17	K	6	Total O 6 6	0	0
17	L	12	Total O 12 12	0	0
17	M	16	Total O 16 16	0	0
17	N	14	Total O 14 14	0	0
17	O	7	Total O 7 7	0	0
17	P	7	Total O 7 7	0	0
17	Q	8	Total O 8 8	0	0
17	R	7	Total O 7 7	0	0
17	S	8	Total O 8 8	0	0
17	T	9	Total O 9 9	0	0
17	U	10	Total O 10 10	0	0
17	V	14	Total O 14 14	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	W	11	Total 11	O 11	0	0
17	X	14	Total 14	O 14	0	0
17	Y	8	Total 8	O 8	0	0
17	Z	19	Total 19	O 19	0	0
17	a	13	Total 13	O 13	0	0
17	b	11	Total 11	O 11	0	0

3 Residue-property plots


These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

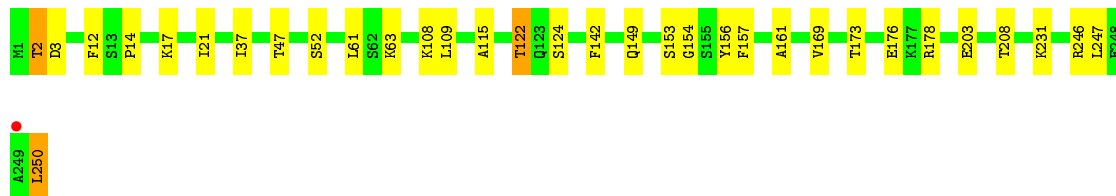
• Molecule 1: Proteasome subunit alpha type-2

Chain A: 




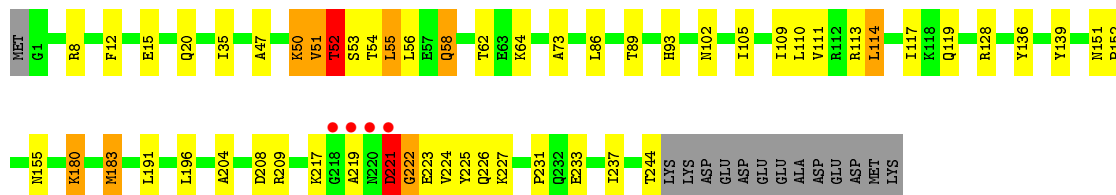
• Molecule 1: Proteasome subunit alpha type-2

Chain O: 



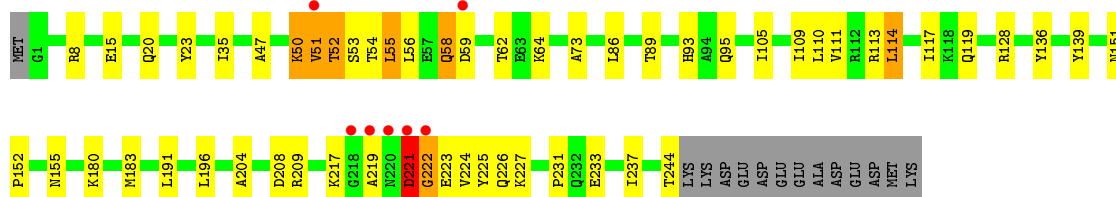
• Molecule 2: Proteasome subunit alpha type-3

Chain B: 

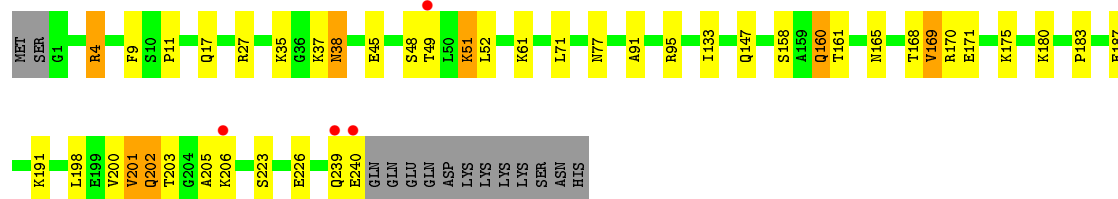
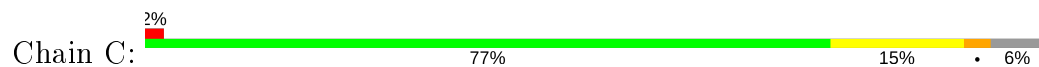


• Molecule 2: Proteasome subunit alpha type-3

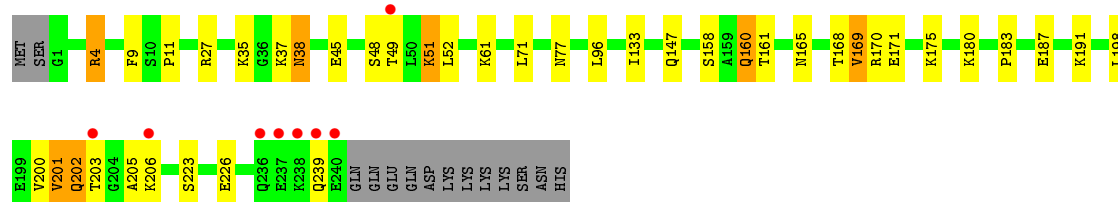
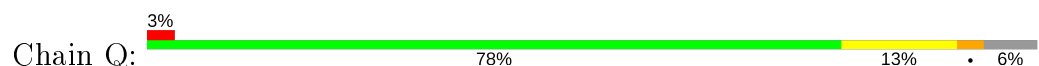
Chain P: 



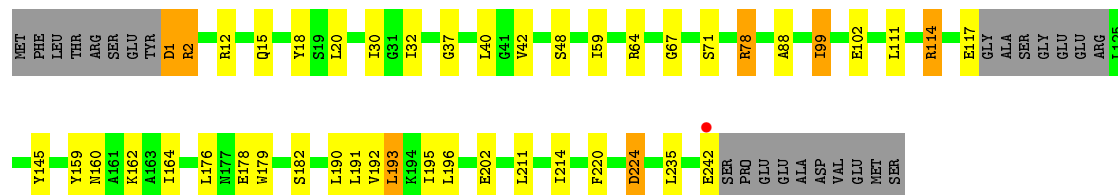
- Molecule 3: Proteasome subunit alpha type-4



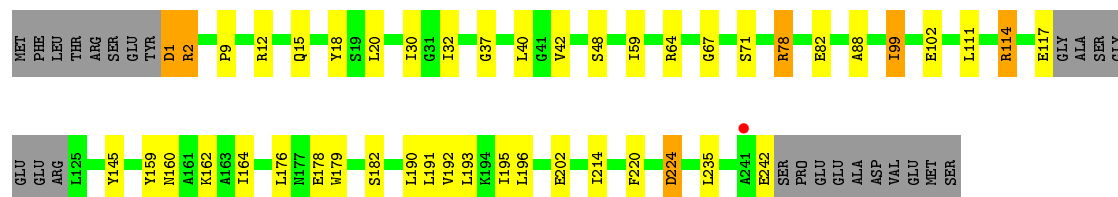
- Molecule 3: Proteasome subunit alpha type-4



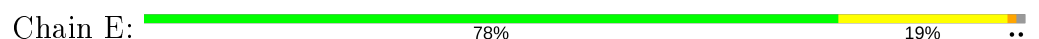
- Molecule 4: Proteasome subunit alpha type-5



- Molecule 4: Proteasome subunit alpha type-5



- Molecule 5: Proteasome subunit alpha type-6





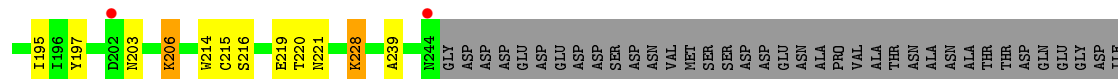
- Molecule 5: Proteasome subunit alpha type-6

Chain S: 78% 19% ..



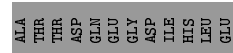
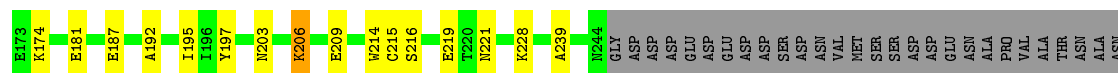
- Molecule 6: Probable proteasome subunit alpha type-7

Chain F: % 70% 13% 16%



- Molecule 6: Probable proteasome subunit alpha type-7

Chain T: 68% 15% 16%

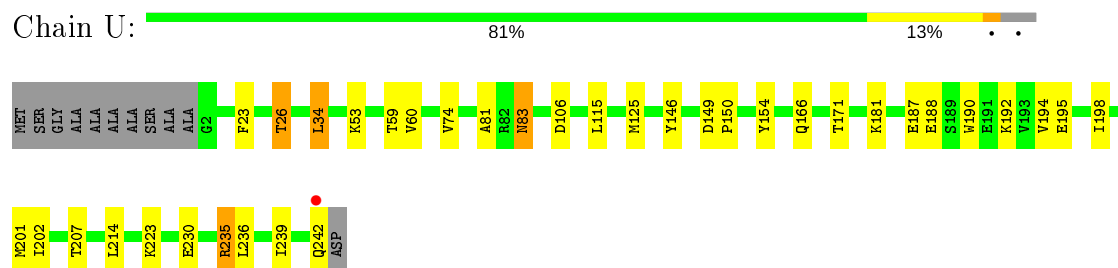


- Molecule 7: Proteasome subunit alpha type-1

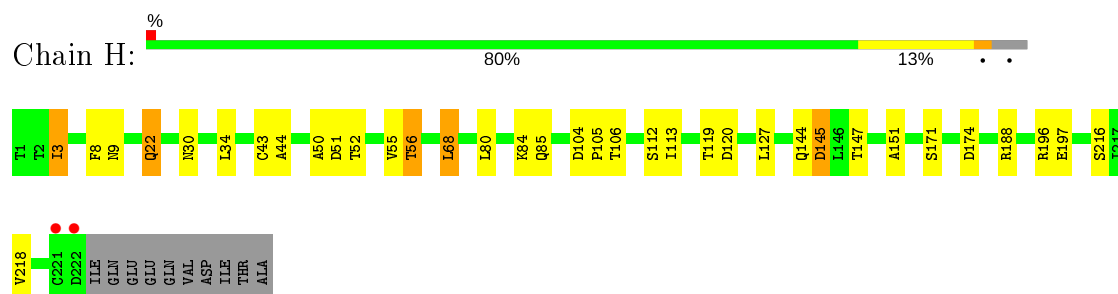
Chain G: 83% 12% . .



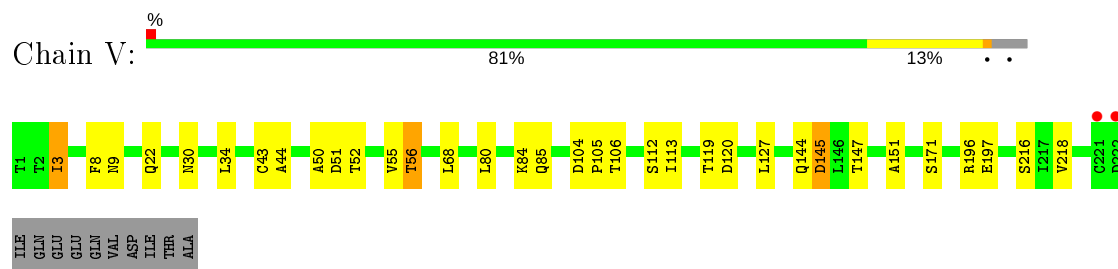
- Molecule 7: Proteasome subunit alpha type-1



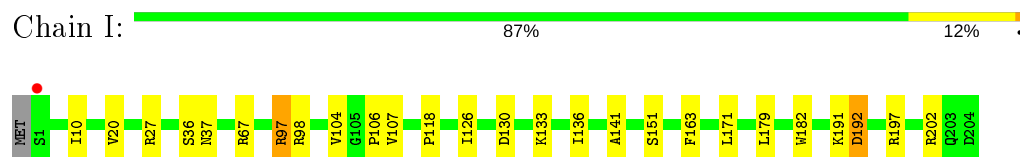
- Molecule 8: Proteasome subunit beta type-2



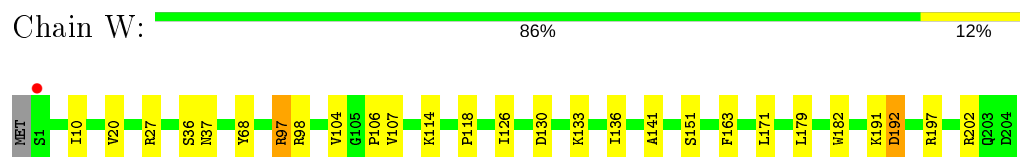
- Molecule 8: Proteasome subunit beta type-2



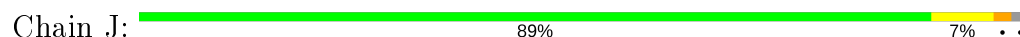
- Molecule 9: Proteasome subunit beta type-3



- Molecule 9: Proteasome subunit beta type-3

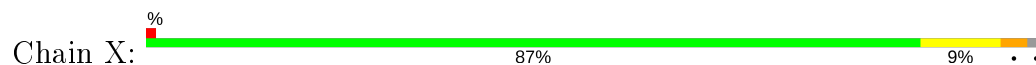


- Molecule 10: Proteasome subunit beta type-4





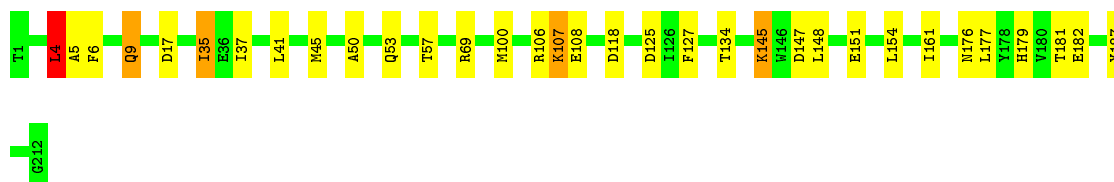
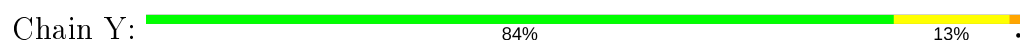
• Molecule 10: Proteasome subunit beta type-4



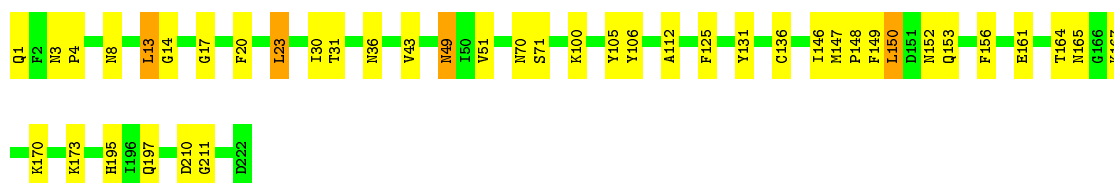
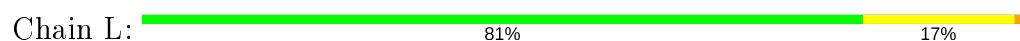
• Molecule 11: Proteasome subunit beta type-5



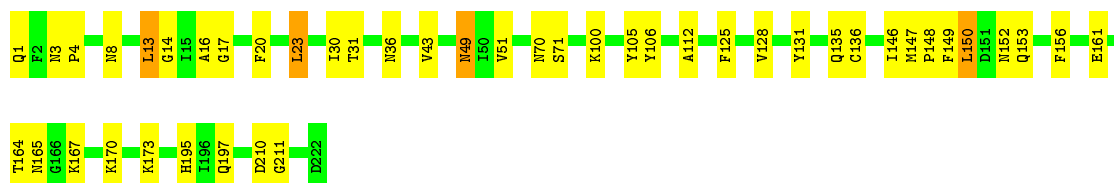
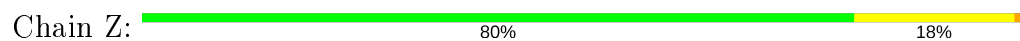
• Molecule 11: Proteasome subunit beta type-5




• Molecule 12: Proteasome subunit beta type-6

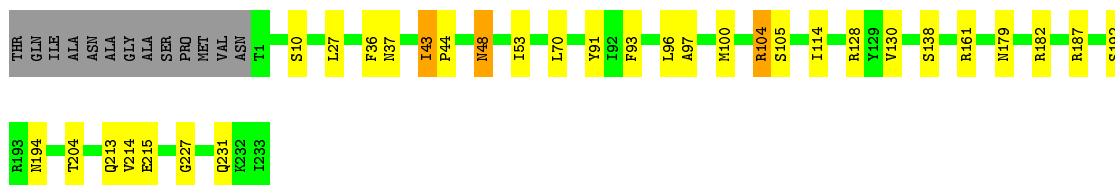


• Molecule 12: Proteasome subunit beta type-6



• Molecule 13: Proteasome subunit beta type-7

Chain M:  82% 12% • 5%




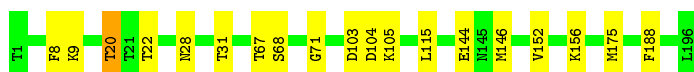
- Molecule 13: Proteasome subunit beta type-7

Chain a:  90% • 5%



- Molecule 14: Proteasome subunit beta type-1

Chain N:  90% 9% •



- Molecule 14: Proteasome subunit beta type-1

Chain b:  % 95% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.45Å 299.75Å 144.52Å 90.00° 112.60° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00 15.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.1 (15.00-3.00) 92.2 (15.00-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 3.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.180 , 0.207 0.182 , 0.206	Depositor DCC
R_{free} test set	9609 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	59.2	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49661	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 2M1

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.30	0/1952	0.58	0/2642
1	O	0.30	0/1952	0.58	0/2642
2	B	0.30	0/1934	0.62	0/2618
2	P	0.30	0/1934	0.62	0/2618
3	C	0.30	0/1910	0.60	0/2586
3	Q	0.29	0/1910	0.60	0/2586
4	D	0.30	0/1837	0.59	0/2475
4	R	0.30	0/1837	0.59	0/2475
5	E	0.29	0/1800	0.58	0/2433
5	S	0.29	0/1800	0.58	0/2433
6	F	0.30	0/1932	0.55	0/2609
6	T	0.30	0/1932	0.55	0/2609
7	G	0.31	0/1945	0.58	0/2634
7	U	0.30	0/1945	0.58	0/2634
8	H	0.28	0/1715	0.59	0/2326
8	V	0.28	0/1715	0.59	0/2326
9	I	0.29	0/1611	0.59	0/2174
9	W	0.30	0/1611	0.59	0/2174
10	J	0.28	0/1589	0.57	0/2142
10	X	0.28	0/1589	0.56	0/2142
11	K	0.31	0/1681	0.61	2/2274 (0.1%)
11	Y	0.31	0/1681	0.61	2/2274 (0.1%)
12	L	0.29	0/1795	0.56	0/2420
12	Z	0.29	0/1795	0.56	0/2420
13	M	0.29	0/1855	0.59	0/2514
13	a	0.29	0/1855	0.59	0/2514
14	N	0.27	0/1541	0.55	0/2087
14	b	0.28	0/1541	0.55	0/2087
All	All	0.29	0/50194	0.58	4/67868 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	I	0	1
9	W	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	4	LEU	CA-CB-CG	5.78	128.58	115.30
11	K	4	LEU	CA-CB-CG	5.71	128.42	115.30
11	Y	145	LYS	CD-CE-NZ	5.05	123.31	111.70
11	K	145	LYS	CD-CE-NZ	5.04	123.29	111.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	192	ASP	Peptide
9	W	192	ASP	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	9	0
1	O	1915	0	1929	14	0
2	B	1904	0	1904	36	0
2	P	1904	0	1904	36	0
3	C	1881	0	1895	28	0
3	Q	1881	0	1895	25	0
4	D	1813	0	1797	19	0
4	R	1813	0	1797	20	0
5	E	1773	0	1775	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	S	1773	0	1775	22	0
6	F	1892	0	1883	21	0
6	T	1892	0	1883	23	0
7	G	1907	0	1901	16	0
7	U	1907	0	1901	18	0
8	H	1684	0	1688	16	0
8	V	1684	0	1688	13	0
9	I	1581	0	1574	14	0
9	W	1581	0	1574	16	0
10	J	1561	0	1569	9	0
10	X	1561	0	1569	13	0
11	K	1644	0	1594	15	0
11	Y	1644	0	1594	19	0
12	L	1757	0	1711	22	0
12	Z	1757	0	1711	25	0
13	M	1824	0	1832	16	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	7	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	H	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	K	38	0	46	0	0
16	Y	38	0	46	0	0
17	A	5	0	0	0	0
17	B	8	0	0	0	0
17	C	4	0	0	0	0
17	D	11	0	0	0	0
17	E	5	0	0	0	0
17	F	11	0	0	0	0
17	G	11	0	0	0	0
17	H	14	0	0	0	0
17	I	7	0	0	0	0
17	J	11	0	0	0	0
17	K	6	0	0	0	0
17	L	12	0	0	0	0
17	M	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	N	14	0	0	0	0
17	O	7	0	0	1	0
17	P	7	0	0	0	0
17	Q	8	0	0	0	0
17	R	7	0	0	0	0
17	S	8	0	0	0	0
17	T	9	0	0	0	0
17	U	10	0	0	0	0
17	V	14	0	0	0	0
17	W	11	0	0	0	0
17	X	14	0	0	0	0
17	Y	8	0	0	0	0
17	Z	19	0	0	0	0
17	a	13	0	0	0	0
17	b	11	0	0	0	0
All	All	49661	0	49158	446	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (446) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.25	1.00
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.25	0.97
11:K:100:MET:CE	11:K:127:PHE:HB2	2.05	0.87
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.56	0.86
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.05	0.86
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.43	0.82
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.58	0.82
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.43	0.81
14:N:20:THR:HG22	14:N:31:THR:OG1	1.83	0.79
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.66	0.78
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.67	0.76
2:B:204:ALA:O	2:B:209:ARG:NH2	2.19	0.76
11:K:53:GLN:O	11:K:57:THR:HG23	1.85	0.76
2:P:204:ALA:O	2:P:209:ARG:NH2	2.19	0.76
11:Y:53:GLN:O	11:Y:57:THR:HG23	1.85	0.75
1:A:176:GLU:HG3	2:B:55:LEU:HD22	1.71	0.73
2:B:93:HIS:HB3	2:B:113:ARG:NH2	2.03	0.73
2:P:93:HIS:HB3	2:P:113:ARG:NH2	2.03	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:23:PHE:O	7:U:26:THR:HB	1.89	0.72
9:W:97:ARG:HH11	9:W:97:ARG:HG2	1.54	0.72
9:I:97:ARG:HG2	9:I:97:ARG:HH11	1.54	0.71
7:G:23:PHE:O	7:G:26:THR:HB	1.91	0.71
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.78	0.65
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.78	0.65
4:R:32:ILE:HD12	4:R:192:VAL:HG23	1.77	0.65
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.97	0.65
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.79	0.64
4:D:32:ILE:HD12	4:D:192:VAL:HG23	1.78	0.64
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.78	0.64
3:C:51:LYS:O	3:C:52:LEU:HB2	1.98	0.63
14:N:20:THR:CG2	14:N:31:THR:OG1	2.46	0.63
11:Y:100:MET:HE3	11:Y:127:PHE:CB	2.29	0.61
3:Q:51:LYS:HA	3:Q:51:LYS:HE3	1.83	0.61
8:H:113:ILE:HG12	8:H:119:THR:HG22	1.83	0.60
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.66	0.60
3:C:51:LYS:HA	3:C:51:LYS:HE3	1.83	0.60
3:Q:160:GLN:HE21	3:Q:161:THR:H	1.50	0.60
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.02	0.60
8:V:113:ILE:HG12	8:V:119:THR:HG22	1.83	0.60
11:K:100:MET:HE1	11:K:127:PHE:HB2	1.82	0.60
3:C:160:GLN:HE21	3:C:161:THR:H	1.50	0.60
12:L:8:ASN:HA	12:L:30:ILE:O	2.02	0.59
5:S:92:ASN:HD21	12:Z:70:ASN:HD21	1.50	0.59
9:W:97:ARG:HG2	9:W:97:ARG:NH1	2.17	0.59
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.68	0.59
2:P:15:GLU:O	3:Q:27:ARG:NH2	2.37	0.58
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.39	0.58
2:B:217:LYS:HD3	2:B:222:GLY:HA2	1.85	0.58
8:V:104:ASP:OD1	8:V:106:THR:HB	2.03	0.58
2:P:217:LYS:HD3	2:P:222:GLY:HA2	1.86	0.58
8:H:104:ASP:OD1	8:H:106:THR:HB	2.04	0.58
12:L:164:THR:O	12:L:165:ASN:HB3	2.04	0.58
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.39	0.57
8:V:3:ILE:HG12	8:V:44:ALA:HB1	1.86	0.57
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.86	0.57
7:G:202:ILE:HG23	7:G:207:THR:O	2.04	0.57
3:C:201:VAL:O	3:C:202:GLN:HB2	2.05	0.57
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.86	0.57
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Z:164:THR:O	12:Z:165:ASN:HB3	2.04	0.57
8:H:3:ILE:HG12	8:H:44:ALA:HB1	1.86	0.57
12:L:17:GLY:HA3	12:L:20:PHE:CE1	2.40	0.57
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.70	0.57
12:Z:17:GLY:HA3	12:Z:20:PHE:CE1	2.40	0.57
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.87	0.56
1:O:12:PHE:H	2:P:20:GLN:HE22	1.53	0.56
8:V:52:THR:O	8:V:56:THR:HB	2.06	0.56
11:K:100:MET:HE3	11:K:127:PHE:CB	2.31	0.56
11:Y:100:MET:HE1	11:Y:127:PHE:HB2	1.85	0.56
6:T:33:SER:HB3	6:T:46:VAL:HG23	1.87	0.56
2:B:155:ASN:ND2	3:C:77:ASN:HB2	2.20	0.56
6:F:33:SER:HB3	6:F:46:VAL:HG23	1.87	0.56
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.88	0.56
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.70	0.55
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.37	0.55
2:P:219:ALA:HB2	2:P:225:TYR:HB2	1.88	0.55
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.36	0.55
8:H:52:THR:O	8:H:56:THR:HB	2.06	0.55
10:J:1:MET:HA	10:J:34:LYS:HE3	1.89	0.55
5:E:9:THR:HG21	5:E:119:THR:HA	1.89	0.55
7:U:202:ILE:HG23	7:U:207:THR:O	2.07	0.55
3:C:201:VAL:HG13	3:C:202:GLN:N	2.23	0.54
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.53	0.54
6:T:34:ILE:HG22	6:T:160:ALA:HB2	1.89	0.54
6:F:34:ILE:HG22	6:F:160:ALA:HB2	1.89	0.54
2:P:139:TYR:CD1	2:P:224:VAL:HG21	2.43	0.54
2:B:219:ALA:HB2	2:B:225:TYR:HB2	1.89	0.54
5:E:163:ARG:HD3	5:E:201:ARG:NH1	2.23	0.54
9:I:97:ARG:NH1	9:I:97:ARG:HG2	2.17	0.54
12:L:4:PRO:O	13:M:104:ARG:NH1	2.38	0.54
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.20	0.53
3:C:71:LEU:HD12	3:C:133:ILE:HG12	1.90	0.53
2:B:139:TYR:CD1	2:B:224:VAL:HG21	2.43	0.53
4:R:30:ILE:HD12	4:R:196:LEU:HG	1.90	0.53
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.23	0.53
5:S:163:ARG:HD3	5:S:201:ARG:NH1	2.23	0.53
3:Q:71:LEU:HD12	3:Q:133:ILE:HG12	1.89	0.53
12:Z:146:ILE:HG22	12:Z:150:LEU:HD22	1.91	0.53
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.55	0.53
10:X:1:MET:HA	10:X:34:LYS:HE3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:154:TRP:CZ3	7:U:60:VAL:HA	2.43	0.53
4:D:224:ASP:N	4:D:224:ASP:OD2	2.42	0.53
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.56	0.53
12:L:161:GLU:HB3	12:L:164:THR:CG2	2.39	0.53
4:R:224:ASP:OD2	4:R:224:ASP:N	2.40	0.53
5:S:9:THR:HG21	5:S:119:THR:HA	1.90	0.53
4:D:30:ILE:HD12	4:D:196:LEU:HG	1.89	0.53
4:R:82:GLU:OE2	11:Y:69:ARG:NH1	2.42	0.52
1:O:122:THR:CG2	2:P:128:ARG:HH21	2.21	0.52
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.91	0.52
12:Z:3:ASN:HD22	12:Z:4:PRO:HD2	1.74	0.52
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.91	0.52
12:L:146:ILE:HG22	12:L:150:LEU:HD22	1.91	0.52
12:L:3:ASN:HD22	12:L:4:PRO:HD2	1.74	0.52
13:M:179:ASN:HD22	13:M:182:ARG:HH11	1.56	0.52
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.56	0.52
6:F:123:ASN:C	6:F:123:ASN:HD22	2.13	0.52
13:M:53:ILE:HG12	13:M:114:ILE:HG12	1.92	0.52
14:N:20:THR:HG23	14:N:28:ASN:HB3	1.90	0.52
12:L:161:GLU:HB3	12:L:164:THR:HG21	1.93	0.51
3:C:9:PHE:H	4:D:15:GLN:HE22	1.57	0.51
12:Z:161:GLU:HB3	12:Z:164:THR:CG2	2.39	0.51
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.58	0.51
9:W:27:ARG:HD3	9:W:179:LEU:O	2.10	0.51
7:G:187:GLU:HG2	7:G:192:LYS:HB2	1.93	0.51
6:T:206:LYS:HA	6:T:206:LYS:HE3	1.92	0.51
12:Z:100:LYS:HD3	12:Z:105:TYR:CE2	2.46	0.51
12:Z:13:LEU:HD12	12:Z:14:GLY:N	2.26	0.51
12:Z:149:PHE:CE1	12:Z:153:GLN:HG3	2.45	0.51
3:C:35:LYS:HG2	3:C:158:SER:O	2.10	0.51
2:P:50:LYS:HE3	2:P:51:VAL:H	1.75	0.51
6:F:206:LYS:HA	6:F:206:LYS:HE3	1.92	0.51
1:O:149:GLN:O	1:O:156:TYR:HA	2.11	0.51
7:G:239:ILE:O	7:G:242:GLN:HB3	2.11	0.51
1:A:149:GLN:O	1:A:156:TYR:HA	2.10	0.50
7:G:188:GLU:OE2	7:G:188:GLU:HA	2.11	0.50
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.42	0.50
12:L:100:LYS:HD3	12:L:105:TYR:CE2	2.46	0.50
7:U:187:GLU:HG2	7:U:192:LYS:HB2	1.93	0.50
9:W:98:ARG:O	9:W:126:ILE:HD11	2.12	0.50
2:B:86:LEU:HB3	2:B:114:LEU:HD21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:LYS:HE3	2:B:51:VAL:H	1.76	0.50
12:L:195:HIS:HD2	12:L:197:GLN:H	1.59	0.50
7:U:188:GLU:OE2	7:U:188:GLU:HA	2.11	0.50
5:E:70:GLY:HA3	5:E:221:PHE:CE2	2.46	0.50
12:L:149:PHE:CE1	12:L:153:GLN:HG3	2.47	0.50
2:P:86:LEU:HB3	2:P:114:LEU:HD21	1.93	0.50
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.11	0.50
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.94	0.50
5:S:70:GLY:HA3	5:S:221:PHE:CE2	2.46	0.50
7:U:239:ILE:O	7:U:242:GLN:HB3	2.11	0.50
9:I:27:ARG:HD3	9:I:179:LEU:O	2.12	0.50
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.42	0.50
10:X:119:ILE:HA	10:X:124:THR:O	2.12	0.50
12:Z:161:GLU:HB3	12:Z:164:THR:HG21	1.93	0.50
5:S:170:TYR:HB2	5:S:198:GLN:HG3	1.94	0.50
3:C:160:GLN:NE2	3:C:161:THR:H	2.10	0.49
3:Q:160:GLN:NE2	3:Q:161:THR:H	2.09	0.49
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.47	0.49
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.47	0.49
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.94	0.49
5:E:170:TYR:HB2	5:E:198:GLN:HG3	1.94	0.49
9:I:104:VAL:HG23	9:I:106:PRO:HD3	1.94	0.49
9:I:98:ARG:O	9:I:126:ILE:HD11	2.12	0.49
12:L:13:LEU:HD12	12:L:14:GLY:N	2.26	0.49
3:C:38:ASN:N	3:C:38:ASN:HD22	2.10	0.49
6:F:36:ILE:HD12	6:F:192:ALA:HB2	1.94	0.49
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.48	0.49
9:W:107:VAL:HG13	9:W:136:ILE:HG21	1.94	0.49
1:A:12:PHE:H	2:B:20:GLN:HE22	1.60	0.49
2:P:155:ASN:ND2	3:Q:77:ASN:HB2	2.28	0.49
2:P:227:LYS:NZ	2:P:233:GLU:OE2	2.46	0.49
6:T:123:ASN:HD22	6:T:123:ASN:C	2.15	0.49
2:B:8:ARG:HD2	3:C:4:ARG:CZ	2.43	0.48
4:D:159:TYR:CZ	4:D:162:LYS:HD3	2.48	0.48
10:J:119:ILE:HA	10:J:124:THR:O	2.12	0.48
3:Q:168:THR:O	3:Q:171:GLU:HB3	2.13	0.48
2:B:12:PHE:H	3:C:17:GLN:HE22	1.61	0.48
7:G:198:ILE:HG23	7:G:214:LEU:HD11	1.95	0.48
12:L:49:ASN:HD21	12:L:211:GLY:HA2	1.77	0.48
4:R:159:TYR:CZ	4:R:162:LYS:HD3	2.48	0.48
6:T:36:ILE:HD12	6:T:192:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:ILE:HD11	2:B:109:ILE:HG22	1.95	0.48
2:B:227:LYS:NZ	2:B:233:GLU:OE2	2.46	0.48
3:C:11:PRO:HA	4:D:18:TYR:CD1	2.49	0.48
2:P:105:ILE:HD11	2:P:109:ILE:HG22	1.96	0.48
6:F:146:MET:HE1	6:F:161:THR:HB	1.96	0.48
8:H:50:ALA:CB	9:I:126:ILE:HG23	2.44	0.48
3:Q:38:ASN:N	3:Q:38:ASN:HD22	2.11	0.48
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.96	0.48
8:V:51:ASP:O	8:V:55:VAL:HG12	2.14	0.48
12:Z:49:ASN:HD21	12:Z:211:GLY:HA2	1.77	0.48
9:W:104:VAL:HG23	9:W:106:PRO:HD3	1.94	0.48
5:E:12:PHE:H	6:F:19:GLN:HE22	1.61	0.48
11:K:6:PHE:HA	11:K:125:ASP:O	2.14	0.48
7:U:149:ASP:HB2	7:U:150:PRO:HD2	1.96	0.48
7:U:198:ILE:HG23	7:U:214:LEU:HD11	1.95	0.48
13:M:182:ARG:HG3	13:M:214:VAL:CG1	2.44	0.48
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.44	0.47
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.95	0.47
2:P:89:THR:HG21	2:P:117:ILE:CD1	2.45	0.47
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.48	0.47
2:B:89:THR:HG21	2:B:117:ILE:CD1	2.44	0.47
10:J:174:MET:HA	10:X:174:MET:HA	1.96	0.47
4:D:37:GLY:HA2	4:D:145:TYR:CE1	2.50	0.47
3:C:168:THR:O	3:C:171:GLU:HB3	2.14	0.47
2:B:58:GLN:HE22	2:B:231:PRO:HB3	1.80	0.47
2:B:8:ARG:HD2	3:C:4:ARG:NH2	2.30	0.47
4:R:67:GLY:HA3	4:R:220:PHE:CD1	2.50	0.47
11:K:5:ALA:HB3	11:K:100:MET:HE2	1.96	0.47
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.15	0.47
2:B:15:GLU:O	3:C:27:ARG:NH2	2.48	0.47
5:S:62:ILE:HG21	5:S:213:ALA:HB2	1.97	0.47
5:E:62:ILE:HG21	5:E:213:ALA:HB2	1.97	0.47
9:I:107:VAL:HG13	9:I:136:ILE:HG21	1.95	0.47
6:T:146:MET:HE1	6:T:161:THR:HB	1.97	0.47
4:R:78:ARG:HD3	4:R:78:ARG:HA	1.74	0.46
6:T:216:SER:HB3	6:T:219:GLU:HB2	1.97	0.46
8:V:80:LEU:HD12	8:V:113:ILE:HD11	1.97	0.46
4:D:67:GLY:HA3	4:D:220:PHE:CD1	2.50	0.46
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.45	0.46
1:A:203:GLU:HB2	1:A:208:THR:HG21	1.97	0.46
3:C:51:LYS:HA	3:C:51:LYS:CE	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:216:SER:HB3	6:F:219:GLU:HB2	1.97	0.46
8:H:51:ASP:O	8:H:55:VAL:HG12	2.15	0.46
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.51	0.46
3:Q:51:LYS:HA	3:Q:51:LYS:CE	2.45	0.46
5:S:68:HIS:HE1	5:S:102:LEU:O	1.99	0.46
4:D:71:SER:HB3	4:D:164:ILE:HD12	1.96	0.46
11:K:4:LEU:HD13	11:K:161:ILE:HD11	1.97	0.46
6:F:197:TYR:CD1	6:F:239:ALA:HB1	2.51	0.46
11:K:179:HIS:CE1	11:K:181:THR:CG2	2.99	0.46
4:R:37:GLY:HA2	4:R:145:TYR:CE1	2.50	0.46
7:G:149:ASP:HB2	7:G:150:PRO:HD2	1.96	0.46
1:O:203:GLU:HB2	1:O:208:THR:HG21	1.97	0.46
6:F:139:LYS:HG2	6:F:139:LYS:O	2.16	0.46
6:T:197:TYR:CD1	6:T:239:ALA:HB1	2.50	0.46
2:B:35:ILE:HD12	2:B:196:LEU:HG	1.98	0.46
11:Y:179:HIS:CE1	11:Y:181:THR:CG2	2.99	0.46
8:H:9:ASN:ND2	8:H:147:THR:HA	2.31	0.46
8:V:9:ASN:ND2	8:V:147:THR:HA	2.30	0.46
6:F:228:LYS:HB2	6:F:228:LYS:HE3	1.80	0.46
7:G:34:LEU:HD23	7:G:34:LEU:C	2.37	0.46
11:K:154:LEU:HD22	11:K:177:LEU:HD13	1.98	0.46
8:V:50:ALA:CB	9:W:126:ILE:HG23	2.46	0.46
5:E:186:ASP:OD2	5:E:231:LYS:HE2	2.16	0.45
4:R:71:SER:HB3	4:R:164:ILE:HD12	1.98	0.45
9:I:20:VAL:CG1	9:I:118:PRO:HB3	2.46	0.45
2:P:58:GLN:HE22	2:P:231:PRO:HB3	1.80	0.45
4:D:111:LEU:O	4:D:114:ARG:HB2	2.17	0.45
9:I:98:ARG:HD2	9:I:126:ILE:CG1	2.46	0.45
9:W:20:VAL:CG1	9:W:118:PRO:HB3	2.46	0.45
9:W:98:ARG:HD2	9:W:126:ILE:CG1	2.46	0.45
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	1.98	0.45
2:P:35:ILE:HD12	2:P:196:LEU:HG	1.99	0.45
11:Y:37:ILE:HB	11:Y:41:LEU:HB3	1.99	0.45
13:M:97:ALA:HA	13:M:130:VAL:HG21	1.99	0.45
2:P:95:GLN:HB3	9:W:68:TYR:CD2	2.52	0.45
5:E:68:HIS:HE1	5:E:102:LEU:O	1.99	0.45
6:F:154:TRP:CZ3	7:G:60:VAL:HA	2.52	0.45
11:K:37:ILE:HB	11:K:41:LEU:HB3	1.98	0.45
8:V:144:GLN:O	8:V:145:ASP:HB2	2.17	0.45
3:C:165:ASN:HB2	3:C:200:VAL:HG11	1.99	0.45
5:E:197:SER:HA	5:E:200:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:144:GLN:O	8:H:145:ASP:HB2	2.17	0.45
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.98	0.45
8:H:84:LYS:HG3	8:H:85:GLN:N	2.32	0.45
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.52	0.45
5:E:178:PHE:HA	5:E:181:ILE:HG13	1.99	0.45
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.98	0.45
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.52	0.45
2:P:73:ALA:HB2	2:P:226:GLN:NE2	2.32	0.45
11:Y:4:LEU:HD13	11:Y:161:ILE:HD11	1.98	0.45
11:Y:107:LYS:HE2	11:Y:108:GLU:HG2	1.99	0.44
3:C:161:THR:HG21	3:C:169:VAL:HG22	1.99	0.44
7:U:223:LYS:HE3	7:U:223:LYS:HB2	1.82	0.44
7:U:34:LEU:C	7:U:34:LEU:HD23	2.37	0.44
11:Y:35:ILE:HB	11:Y:45:MET:HE3	1.99	0.44
4:D:78:ARG:HD3	4:D:78:ARG:HA	1.74	0.44
13:M:194:ASN:ND2	13:M:213:GLN:HG2	2.33	0.44
3:C:198:LEU:HA	3:C:201:VAL:HG12	2.00	0.44
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.53	0.44
5:S:197:SER:HA	5:S:200:LEU:HD12	1.99	0.44
6:F:146:MET:CE	6:F:161:THR:HB	2.48	0.44
12:Z:51:VAL:HG23	12:Z:112:ALA:HB3	2.00	0.44
12:L:51:VAL:HG23	12:L:112:ALA:HB3	1.99	0.44
6:T:139:LYS:HG2	6:T:139:LYS:O	2.17	0.44
7:U:195:GLU:HG3	7:U:235:ARG:HG3	2.00	0.44
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	2.00	0.44
11:Y:154:LEU:HD22	11:Y:177:LEU:HD13	2.00	0.44
11:K:107:LYS:HG3	11:K:108:GLU:HG3	2.00	0.44
4:R:111:LEU:O	4:R:114:ARG:HB2	2.18	0.44
5:S:186:ASP:OD2	5:S:231:LYS:HE2	2.17	0.44
7:G:195:GLU:HG3	7:G:235:ARG:HG3	2.00	0.44
7:G:223:LYS:HB2	7:G:223:LYS:HE3	1.82	0.44
7:G:83:ASN:C	7:G:83:ASN:HD22	2.21	0.44
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	2.00	0.44
3:Q:96:LEU:HD11	10:X:58:GLU:HB3	2.00	0.44
4:R:191:LEU:O	4:R:195:ILE:HG13	2.18	0.44
11:K:176:ASN:ND2	11:K:187:TYR:OH	2.51	0.43
3:Q:165:ASN:HB2	3:Q:200:VAL:HG11	2.00	0.43
2:B:73:ALA:HB2	2:B:226:GLN:NE2	2.33	0.43
6:T:146:MET:CE	6:T:161:THR:HB	2.48	0.43
11:Y:5:ALA:HB3	11:Y:100:MET:HE2	2.00	0.43
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:58:GLN:NE2	2:B:231:PRO:HB3	2.33	0.43
3:Q:161:THR:HG21	3:Q:169:VAL:HG22	2.00	0.43
5:S:178:PHE:HA	5:S:181:ILE:HG13	1.99	0.43
8:V:84:LYS:HG3	8:V:85:GLN:N	2.32	0.43
8:V:8:PHE:HB3	8:V:151:ALA:HB2	2.01	0.43
2:B:110:LEU:HD23	2:B:110:LEU:C	2.39	0.43
12:Z:156:PHE:CG	12:Z:170:LYS:HD3	2.53	0.43
4:D:191:LEU:O	4:D:195:ILE:HG13	2.18	0.43
6:T:34:ILE:HG22	6:T:160:ALA:CB	2.48	0.43
2:B:111:VAL:HG22	2:B:136:TYR:CG	2.54	0.43
4:D:159:TYR:CE2	5:E:56:SER:HB3	2.53	0.43
11:K:107:LYS:HE2	11:K:108:GLU:HG2	2.00	0.43
13:M:27:LEU:HB2	13:M:192:SER:HB3	2.00	0.43
14:N:152:VAL:HA	14:N:175:MET:HE1	2.00	0.43
9:I:163:PHE:CE1	9:I:197:ARG:HD2	2.53	0.43
9:W:163:PHE:CE1	9:W:197:ARG:HD2	2.54	0.43
3:C:51:LYS:HE3	3:C:52:LEU:H	1.84	0.43
2:P:58:GLN:NE2	2:P:231:PRO:HB3	2.34	0.43
4:D:42:VAL:HG22	4:D:59:ILE:HD11	2.01	0.43
7:G:106:ASP:HB3	7:G:146:TYR:CZ	2.54	0.43
5:E:98:PHE:O	13:M:91:TYR:HA	2.18	0.43
2:P:111:VAL:HG22	2:P:136:TYR:CG	2.54	0.43
5:S:112:CYS:SG	6:T:82:ARG:HD3	2.59	0.43
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	2.01	0.43
12:Z:152:ASN:O	12:Z:156:PHE:HA	2.19	0.43
2:B:52:THR:HG23	2:B:53:SER:O	2.19	0.42
8:H:8:PHE:HB3	8:H:151:ALA:HB2	2.00	0.42
10:J:36:ARG:HD3	10:J:36:ARG:HA	1.82	0.42
5:S:170:TYR:C	5:S:170:TYR:CD1	2.92	0.42
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.34	0.42
5:E:134:ILE:HD12	5:E:215:VAL:HG12	2.01	0.42
10:J:173:PRO:HB3	10:X:22:THR:HG21	2.01	0.42
12:L:152:ASN:O	12:L:156:PHE:HA	2.19	0.42
11:K:145:LYS:HB2	11:K:148:LEU:HD13	2.01	0.42
2:P:58:GLN:NE2	2:P:208:ASP:HA	2.35	0.42
1:O:176:GLU:HG3	2:P:55:LEU:HD22	2.01	0.42
4:R:178:GLU:HB2	4:R:191:LEU:HD21	2.01	0.42
10:X:25:ILE:HD11	11:Y:134:THR:HG21	2.00	0.42
2:B:89:THR:HG21	2:B:117:ILE:HD13	2.02	0.42
2:P:110:LEU:C	2:P:110:LEU:HD23	2.40	0.42
1:A:247:LEU:O	1:A:250:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:1:MET:HA	10:J:34:LYS:CE	2.49	0.42
1:O:247:LEU:O	1:O:250:LEU:HB2	2.19	0.42
10:X:1:MET:HA	10:X:34:LYS:CE	2.50	0.42
6:F:34:ILE:HG22	6:F:160:ALA:CB	2.48	0.42
12:L:147:MET:N	12:L:148:PRO:HD2	2.34	0.42
2:P:221:ASP:O	2:P:223:GLU:N	2.53	0.42
3:Q:51:LYS:HE3	3:Q:52:LEU:H	1.85	0.42
6:T:105:ILE:HG21	6:T:143:HIS:HB2	2.01	0.42
3:C:160:GLN:HE21	3:C:160:GLN:CA	2.33	0.42
6:F:172:LEU:HD12	6:F:195:ILE:HD13	2.01	0.42
7:G:74:VAL:HG11	7:G:81:ALA:CB	2.50	0.42
9:I:36:SER:HB2	10:J:126:VAL:HG11	2.01	0.42
4:R:42:VAL:HG22	4:R:59:ILE:HD11	2.01	0.42
7:U:83:ASN:C	7:U:83:ASN:HD22	2.23	0.42
1:O:142:PHE:CE2	9:W:114:LYS:HD3	2.55	0.42
10:X:162:LYS:HB3	10:X:162:LYS:HE2	1.87	0.42
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.52	0.42
13:M:27:LEU:HD12	13:M:36:PHE:O	2.20	0.42
13:M:48:ASN:H	13:M:48:ASN:HD22	1.66	0.42
2:P:52:THR:HG23	2:P:53:SER:O	2.18	0.42
5:S:153:THR:HG21	6:T:55:LEU:CD2	2.49	0.42
6:T:155:GLY:HA3	7:U:59:THR:HG21	2.02	0.42
5:S:136:TYR:CE1	5:S:217:LYS:HA	2.55	0.42
5:S:45:LEU:HB2	5:S:213:ALA:HB3	2.02	0.42
9:W:97:ARG:CG	9:W:97:ARG:HH11	2.30	0.42
13:M:96:LEU:O	13:M:100:MET:HG2	2.20	0.42
6:T:41:GLY:HA3	6:T:215:CYS:O	2.20	0.42
12:Z:164:THR:O	12:Z:165:ASN:CB	2.68	0.42
3:C:91:ALA:O	3:C:95:ARG:HG3	2.20	0.41
4:D:178:GLU:HB2	4:D:191:LEU:HD21	2.01	0.41
6:F:105:ILE:N	6:F:106:PRO:CD	2.83	0.41
12:L:156:PHE:CG	12:L:170:LYS:HD3	2.54	0.41
5:S:207:VAL:HG22	5:S:226:GLY:O	2.20	0.41
6:T:172:LEU:HD12	6:T:195:ILE:HD13	2.00	0.41
8:V:112:SER:OG	8:V:120:ASP:HB2	2.19	0.41
10:X:36:ARG:HD3	10:X:36:ARG:HA	1.83	0.41
2:B:221:ASP:O	2:B:223:GLU:N	2.53	0.41
5:E:136:TYR:CE1	5:E:217:LYS:HA	2.55	0.41
5:E:78:PRO:O	5:E:81:ARG:HB3	2.20	0.41
13:M:43:ILE:HD11	13:M:53:ILE:HD12	2.02	0.41
6:T:105:ILE:N	6:T:106:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:170:TYR:C	5:E:170:TYR:CD1	2.93	0.41
6:F:105:ILE:HG21	6:F:143:HIS:HB2	2.01	0.41
2:B:180:LYS:O	2:B:183:MET:HB2	2.20	0.41
3:C:223:SER:OG	3:C:226:GLU:HG3	2.20	0.41
7:G:187:GLU:CG	7:G:192:LYS:HB2	2.51	0.41
2:B:102:ASN:ND2	9:I:67:ARG:HH12	2.18	0.41
1:A:90:ARG:HD3	8:H:68:LEU:HD23	2.02	0.41
13:M:93:PHE:CE2	13:M:128:ARG:HD3	2.56	0.41
1:O:37:ILE:HG23	1:O:161:ALA:HB2	2.02	0.41
7:U:106:ASP:HB3	7:U:146:TYR:CZ	2.55	0.41
9:W:36:SER:HB2	10:X:126:VAL:HG11	2.02	0.41
8:H:174:ASP:OD2	8:H:188:ARG:NH1	2.52	0.41
13:M:227:GLY:HA3	13:M:231:GLN:HB3	2.02	0.41
14:N:8:PHE:HB2	14:N:146:MET:O	2.21	0.41
1:O:21:ILE:HG21	1:O:153:SER:HB3	2.02	0.41
2:P:8:ARG:HD2	3:Q:4:ARG:NH2	2.36	0.41
11:Y:50:ALA:CB	12:Z:128:VAL:HG23	2.51	0.41
12:Z:16:ALA:O	12:Z:135:GLN:NE2	2.52	0.41
5:E:207:VAL:HG22	5:E:226:GLY:O	2.20	0.41
6:F:123:ASN:HD22	6:F:124:SER:N	2.19	0.41
14:N:67:THR:HA	14:N:71:GLY:O	2.21	0.41
4:R:9:PRO:HA	5:S:23:TYR:CG	2.56	0.41
5:S:134:ILE:HD12	5:S:215:VAL:HG12	2.01	0.41
5:S:78:PRO:O	5:S:81:ARG:HB3	2.21	0.41
2:B:58:GLN:NE2	2:B:208:ASP:HA	2.35	0.41
5:E:45:LEU:HB2	5:E:213:ALA:HB3	2.03	0.41
6:F:41:GLY:HA3	6:F:215:CYS:O	2.21	0.41
14:N:156:LYS:HE2	14:N:188:PHE:CD1	2.56	0.41
3:Q:223:SER:OG	3:Q:226:GLU:HG3	2.20	0.41
7:U:74:VAL:HG11	7:U:81:ALA:CB	2.50	0.41
13:M:43:ILE:HA	13:M:44:PRO:HD3	1.84	0.41
2:P:93:HIS:CG	2:P:113:ARG:HE	2.39	0.41
2:P:59:ASP:HB3	2:P:231:PRO:HG2	2.03	0.41
4:R:1:ASP:O	4:R:2:ARG:CB	2.69	0.41
1:A:37:ILE:HG23	1:A:161:ALA:HB2	2.02	0.41
6:F:216:SER:H	6:F:220:THR:HG1	1.67	0.41
8:H:22:GLN:HB2	8:H:22:GLN:HE21	1.72	0.41
1:O:108:LYS:HG2	17:O:301:HOH:O	2.21	0.41
2:P:50:LYS:O	2:P:52:THR:N	2.54	0.41
7:U:190:TRP:O	7:U:194:VAL:HG23	2.21	0.41
5:E:180:LYS:HE3	5:E:180:LYS:HB2	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:123:ASN:HD22	6:T:124:SER:N	2.19	0.41
3:C:45:GLU:HG3	3:C:201:VAL:HG23	2.04	0.40
13:M:104:ARG:HG3	13:M:105:SER:N	2.35	0.40
4:D:1:ASP:O	4:D:2:ARG:CB	2.69	0.40
5:S:104:VAL:HG12	5:S:144:LEU:HD22	2.03	0.40
2:P:89:THR:HG21	2:P:117:ILE:HD13	2.02	0.40
10:X:35:THR:HG21	10:X:182:LYS:HZ2	1.87	0.40
12:Z:147:MET:N	12:Z:148:PRO:CD	2.85	0.40
8:H:112:SER:OG	8:H:120:ASP:HB2	2.21	0.40
2:B:50:LYS:O	2:B:52:THR:N	2.54	0.40
4:D:193:LEU:HD22	4:D:211:LEU:HD11	2.04	0.40
5:E:197:SER:HA	5:E:200:LEU:CD1	2.52	0.40
1:O:115:ALA:HB1	1:O:154:GLY:O	2.21	0.40
1:O:47:THR:HG21	1:O:63:LYS:HE2	2.04	0.40
3:Q:45:GLU:HG3	3:Q:201:VAL:HG23	2.03	0.40
6:T:87:ARG:HG2	6:T:115:TYR:CD1	2.57	0.40
6:T:50:ILE:HD11	6:T:209:GLU:HB2	2.04	0.40
7:U:187:GLU:CG	7:U:192:LYS:HB2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	236 (95%)	11 (4%)	1 (0%)	34	72
1	O	248/250 (99%)	236 (95%)	11 (4%)	1 (0%)	34	72
2	B	242/258 (94%)	226 (93%)	11 (4%)	5 (2%)	7	33
2	P	242/258 (94%)	226 (93%)	11 (4%)	5 (2%)	7	33
3	C	238/254 (94%)	224 (94%)	8 (3%)	6 (2%)	5	28
3	Q	238/254 (94%)	224 (94%)	8 (3%)	6 (2%)	5	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	231/260 (89%)	225 (97%)	4 (2%)	2 (1%)	17	55
4	R	231/260 (89%)	225 (97%)	4 (2%)	2 (1%)	17	55
5	E	229/234 (98%)	210 (92%)	17 (7%)	2 (1%)	17	55
5	S	229/234 (98%)	210 (92%)	17 (7%)	2 (1%)	17	55
6	F	241/288 (84%)	230 (95%)	11 (5%)	0	100	100
6	T	241/288 (84%)	230 (95%)	11 (5%)	0	100	100
7	G	239/252 (95%)	231 (97%)	8 (3%)	0	100	100
7	U	239/252 (95%)	231 (97%)	8 (3%)	0	100	100
8	H	220/232 (95%)	208 (94%)	10 (4%)	2 (1%)	17	55
8	V	220/232 (95%)	208 (94%)	10 (4%)	2 (1%)	17	55
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	188 (97%)	3 (2%)	2 (1%)	15	53
10	X	193/198 (98%)	188 (97%)	3 (2%)	2 (1%)	15	53
11	K	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	29	68
11	Y	210/212 (99%)	203 (97%)	6 (3%)	1 (0%)	29	68
12	L	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
12	Z	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
13	M	231/246 (94%)	219 (95%)	12 (5%)	0	100	100
13	a	231/246 (94%)	219 (95%)	12 (5%)	0	100	100
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
All	All	6276/6614 (95%)	5986 (95%)	248 (4%)	42 (1%)	22	60

All (42) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
2	B	52	THR
2	B	183	MET
3	C	202	GLN
3	C	205	ALA
4	D	2	ARG

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Mol	Chain	Res	Type
1	O	2	THR
2	P	51	VAL
2	P	52	THR
2	P	183	MET
3	Q	202	GLN
3	Q	205	ALA
4	R	2	ARG
2	B	222	GLY
4	D	114	ARG
5	E	231	LYS
10	J	2	ASP
2	P	222	GLY
4	R	114	ARG
5	S	231	LYS
10	X	2	ASP
3	C	49	THR
3	Q	49	THR
8	H	145	ASP
8	H	171	SER
11	K	9	GLN
8	V	145	ASP
8	V	171	SER
11	Y	9	GLN
2	B	221	ASP
3	C	183	PRO
2	P	221	ASP
3	Q	183	PRO
3	Q	206	LYS
3	C	206	LYS
3	C	201	VAL
3	Q	201	VAL
10	J	9	VAL
10	X	9	VAL
5	E	185	PRO
5	S	185	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	194 (93%)	15 (7%)	14	45
1	O	209/209 (100%)	194 (93%)	15 (7%)	14	45
2	B	203/216 (94%)	189 (93%)	14 (7%)	15	48
2	P	203/216 (94%)	190 (94%)	13 (6%)	17	51
3	C	212/226 (94%)	196 (92%)	16 (8%)	13	43
3	Q	212/226 (94%)	197 (93%)	15 (7%)	14	46
4	D	194/215 (90%)	175 (90%)	19 (10%)	8	30
4	R	194/215 (90%)	175 (90%)	19 (10%)	8	30
5	E	190/193 (98%)	173 (91%)	17 (9%)	9	35
5	S	190/193 (98%)	173 (91%)	17 (9%)	9	35
6	F	201/239 (84%)	182 (90%)	19 (10%)	8	32
6	T	201/239 (84%)	182 (90%)	19 (10%)	8	32
7	G	206/210 (98%)	192 (93%)	14 (7%)	16	48
7	U	206/210 (98%)	192 (93%)	14 (7%)	16	48
8	H	181/190 (95%)	169 (93%)	12 (7%)	16	49
8	V	181/190 (95%)	169 (93%)	12 (7%)	16	49
9	I	172/173 (99%)	162 (94%)	10 (6%)	20	55
9	W	172/173 (99%)	162 (94%)	10 (6%)	20	55
10	J	173/175 (99%)	165 (95%)	8 (5%)	27	64
10	X	173/175 (99%)	165 (95%)	8 (5%)	27	64
11	K	169/169 (100%)	159 (94%)	10 (6%)	19	54
11	Y	169/169 (100%)	159 (94%)	10 (6%)	19	54
12	L	185/185 (100%)	174 (94%)	11 (6%)	19	54
12	Z	185/185 (100%)	174 (94%)	11 (6%)	19	54
13	M	199/208 (96%)	188 (94%)	11 (6%)	21	57
13	a	199/208 (96%)	188 (94%)	11 (6%)	21	57
14	N	162/162 (100%)	153 (94%)	9 (6%)	21	56
14	b	162/162 (100%)	153 (94%)	9 (6%)	21	56
All	All	5312/5540 (96%)	4944 (93%)	368 (7%)	15	48

All (368) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	3	ASP
1	A	17	LYS
1	A	52	SER
1	A	61	LEU
1	A	109	LEU
1	A	122	THR
1	A	124	SER
1	A	157	PHE
1	A	169	VAL
1	A	173	THR
1	A	178	ARG
1	A	231	LYS
1	A	246	ARG
1	A	250	LEU
2	B	50	LYS
2	B	52	THR
2	B	54	THR
2	B	55	LEU
2	B	56	LEU
2	B	58	GLN
2	B	62	THR
2	B	114	LEU
2	B	119	GLN
2	B	180	LYS
2	B	191	LEU
2	B	221	ASP
2	B	237	ILE
2	B	244	THR
3	C	4	ARG
3	C	37	LYS
3	C	38	ASN
3	C	48	SER
3	C	51	LYS
3	C	61	LYS
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	175	LYS
3	C	180	LYS
3	C	187	GLU
3	C	191	LYS
3	C	203	THR

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Mol	Chain	Res	Type
3	C	239	GLN
3	C	240	GLU
4	D	1	ASP
4	D	12	ARG
4	D	20	LEU
4	D	40	LEU
4	D	48	SER
4	D	64	ARG
4	D	78	ARG
4	D	99	ILE
4	D	102	GLU
4	D	117	GLU
4	D	176	LEU
4	D	182	SER
4	D	190	LEU
4	D	193	LEU
4	D	202	GLU
4	D	214	ILE
4	D	224	ASP
4	D	235	LEU
4	D	242	GLU
5	E	9	THR
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	60	LYS
5	E	61	LYS
5	E	71	LEU
5	E	87	LEU
5	E	144	LEU
5	E	174	THR
5	E	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	211	SER
5	E	231	LYS
6	F	51	THR
6	F	59	LYS
6	F	94	SER
6	F	96	LYS

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Mol	Chain	Res	Type
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	148	GLU
6	F	165	ARG
6	F	167	SER
6	F	172	LEU
6	F	174	LYS
6	F	181	GLU
6	F	187	GLU
6	F	203	ASN
6	F	206	LYS
6	F	214	TRP
6	F	221	ASN
6	F	228	LYS
7	G	26	THR
7	G	34	LEU
7	G	53	LYS
7	G	83	ASN
7	G	115	LEU
7	G	125	MET
7	G	154	TYR
7	G	166	GLN
7	G	171	THR
7	G	181	LYS
7	G	201	MET
7	G	230	GLU
7	G	235	ARG
7	G	236	LEU
8	H	3	ILE
8	H	22	GLN
8	H	30	ASN
8	H	34	LEU
8	H	43	CYS
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
8	H	197	GLU
8	H	216	SER
8	H	218	VAL
9	I	37	ASN

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Mol	Chain	Res	Type
9	I	97	ARG
9	I	130	ASP
9	I	133	LYS
9	I	151	SER
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	192	ASP
9	I	202	ARG
10	J	2	ASP
10	J	23	ARG
10	J	35	THR
10	J	36	ARG
10	J	75	LEU
10	J	78	GLN
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	9	GLN
11	K	17	ASP
11	K	35	ILE
11	K	106	ARG
11	K	107	LYS
11	K	118	ASP
11	K	147	ASP
11	K	151	GLU
11	K	182	GLU
12	L	1	GLN
12	L	13	LEU
12	L	23	LEU
12	L	49	ASN
12	L	71	SER
12	L	106	TYR
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
12	L	173	LYS
12	L	210	ASP
13	M	10	SER
13	M	37	ASN
13	M	43	ILE
13	M	48	ASN

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Mol	Chain	Res	Type
13	M	70	LEU
13	M	104	ARG
13	M	138	SER
13	M	161	ARG
13	M	187	ARG
13	M	204	THR
13	M	215	GLU
14	N	9	LYS
14	N	20	THR
14	N	22	THR
14	N	68	SER
14	N	103	ASP
14	N	104	ASP
14	N	105	LYS
14	N	115	LEU
14	N	144	GLU
1	O	2	THR
1	O	3	ASP
1	O	17	LYS
1	O	52	SER
1	O	61	LEU
1	O	109	LEU
1	O	122	THR
1	O	124	SER
1	O	157	PHE
1	O	169	VAL
1	O	173	THR
1	O	178	ARG
1	O	231	LYS
1	O	246	ARG
1	O	250	LEU
2	P	50	LYS
2	P	54	THR
2	P	55	LEU
2	P	56	LEU
2	P	58	GLN
2	P	62	THR
2	P	114	LEU
2	P	119	GLN
2	P	180	LYS
2	P	191	LEU
2	P	221	ASP

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Mol	Chain	Res	Type
2	P	237	ILE
2	P	244	THR
3	Q	4	ARG
3	Q	37	LYS
3	Q	38	ASN
3	Q	48	SER
3	Q	51	LYS
3	Q	61	LYS
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	175	LYS
3	Q	180	LYS
3	Q	187	GLU
3	Q	191	LYS
3	Q	203	THR
3	Q	239	GLN
4	R	1	ASP
4	R	12	ARG
4	R	20	LEU
4	R	40	LEU
4	R	48	SER
4	R	64	ARG
4	R	78	ARG
4	R	99	ILE
4	R	102	GLU
4	R	117	GLU
4	R	176	LEU
4	R	182	SER
4	R	190	LEU
4	R	193	LEU
4	R	202	GLU
4	R	214	ILE
4	R	224	ASP
4	R	235	LEU
4	R	242	GLU
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	55	LEU

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Mol	Chain	Res	Type
5	S	60	LYS
5	S	61	LYS
5	S	71	LEU
5	S	87	LEU
5	S	144	LEU
5	S	174	THR
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	211	SER
5	S	231	LYS
6	T	51	THR
6	T	59	LYS
6	T	94	SER
6	T	96	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	148	GLU
6	T	165	ARG
6	T	167	SER
6	T	172	LEU
6	T	174	LYS
6	T	181	GLU
6	T	187	GLU
6	T	203	ASN
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
6	T	228	LYS
7	U	26	THR
7	U	34	LEU
7	U	53	LYS
7	U	83	ASN
7	U	115	LEU
7	U	125	MET
7	U	154	TYR
7	U	166	GLN
7	U	171	THR
7	U	181	LYS
7	U	201	MET
7	U	230	GLU

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Mol	Chain	Res	Type
7	U	235	ARG
7	U	236	LEU
8	V	3	ILE
8	V	22	GLN
8	V	30	ASN
8	V	34	LEU
8	V	43	CYS
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
8	V	197	GLU
8	V	216	SER
8	V	218	VAL
9	W	37	ASN
9	W	97	ARG
9	W	130	ASP
9	W	133	LYS
9	W	151	SER
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
9	W	202	ARG
10	X	2	ASP
10	X	23	ARG
10	X	35	THR
10	X	36	ARG
10	X	75	LEU
10	X	78	GLN
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	9	GLN
11	Y	17	ASP
11	Y	35	ILE
11	Y	106	ARG
11	Y	107	LYS
11	Y	118	ASP
11	Y	147	ASP
11	Y	151	GLU
11	Y	182	GLU

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Mol	Chain	Res	Type
12	Z	1	GLN
12	Z	13	LEU
12	Z	23	LEU
12	Z	49	ASN
12	Z	71	SER
12	Z	106	TYR
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
12	Z	173	LYS
12	Z	210	ASP
13	a	10	SER
13	a	37	ASN
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	138	SER
13	a	161	ARG
13	a	187	ARG
13	a	204	THR
13	a	215	GLU
14	b	9	LYS
14	b	20	THR
14	b	22	THR
14	b	68	SER
14	b	103	ASP
14	b	104	ASP
14	b	105	LYS
14	b	115	LEU
14	b	144	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (129) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	58	GLN
2	B	95	GLN
2	B	102	ASN
2	B	119	GLN
2	B	123	GLN

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Mol	Chain	Res	Type
2	B	155	ASN
2	B	226	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	146	GLN
4	D	210	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	120	GLN
5	E	209	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	191	GLN
6	F	240	GLN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
7	G	175	ASN
8	H	22	GLN
8	H	66	HIS
8	H	172	ASN
8	H	200	GLN
9	I	31	GLN
10	J	55	GLN
10	J	118	GLN
10	J	191	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
12	L	1	GLN
12	L	3	ASN
12	L	36	ASN

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Mol	Chain	Res	Type
12	L	49	ASN
12	L	70	ASN
12	L	80	ASN
12	L	158	ASN
12	L	195	HIS
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	161	GLN
1	O	94	HIS
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	155	ASN
2	P	176	GLN
2	P	226	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	146	GLN
4	R	210	GLN
4	R	225	ASN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	209	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	191	GLN
6	T	203	ASN

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Mol	Chain	Res	Type
6	T	240	GLN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	167	GLN
7	U	175	ASN
8	V	22	GLN
8	V	66	HIS
8	V	144	GLN
8	V	172	ASN
8	V	200	GLN
9	W	31	GLN
9	W	71	ASN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
10	X	191	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	1	GLN
12	Z	3	ASN
12	Z	36	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	80	ASN
12	Z	158	ASN
12	Z	195	HIS
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	179	ASN
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	2M1	K	301	11	38,38,38	1.49	5 (13%)	49,51,51	1.33	5 (10%)
16	2M1	Y	301	11	38,38,38	1.43	5 (13%)	49,51,51	1.35	6 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	2M1	K	301	11	-	6/43/43/43	0/1/1/1
16	2M1	Y	301	11	-	5/43/43/43	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	K	301	2M1	C26-S42	4.21	1.84	1.78
16	K	301	2M1	O43-S42	4.13	1.53	1.44
16	Y	301	2M1	C5-C4	-4.00	1.41	1.50
16	Y	301	2M1	O43-S42	3.90	1.53	1.44
16	K	301	2M1	C5-C4	-3.88	1.41	1.50
16	K	301	2M1	O44-S42	3.87	1.52	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Y	301	2M1	O44-S42	3.84	1.52	1.44
16	Y	301	2M1	C26-S42	3.61	1.83	1.78
16	K	301	2M1	C41-C26	2.57	1.55	1.52
16	Y	301	2M1	C41-C26	2.30	1.55	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Y	301	2M1	O6-C7-N9	4.81	120.29	110.50
16	K	301	2M1	O6-C7-N9	4.49	119.62	110.50
16	Y	301	2M1	O44-S42-O43	-3.75	109.09	117.09
16	K	301	2M1	O43-S42-C26	3.69	110.93	108.34
16	K	301	2M1	O44-S42-O43	-3.45	109.72	117.09
16	Y	301	2M1	O43-S42-C26	3.00	110.45	108.34
16	Y	301	2M1	O8-C7-N9	-2.67	120.47	124.85
16	Y	301	2M1	O6-C7-O8	-2.61	119.25	124.25
16	K	301	2M1	O8-C7-N9	-2.56	120.65	124.85
16	Y	301	2M1	C5-O6-C7	-2.50	110.34	115.93
16	K	301	2M1	O6-C7-O8	-2.36	119.72	124.25

There are no chirality outliers.

All (11) torsion outliers are listed below:

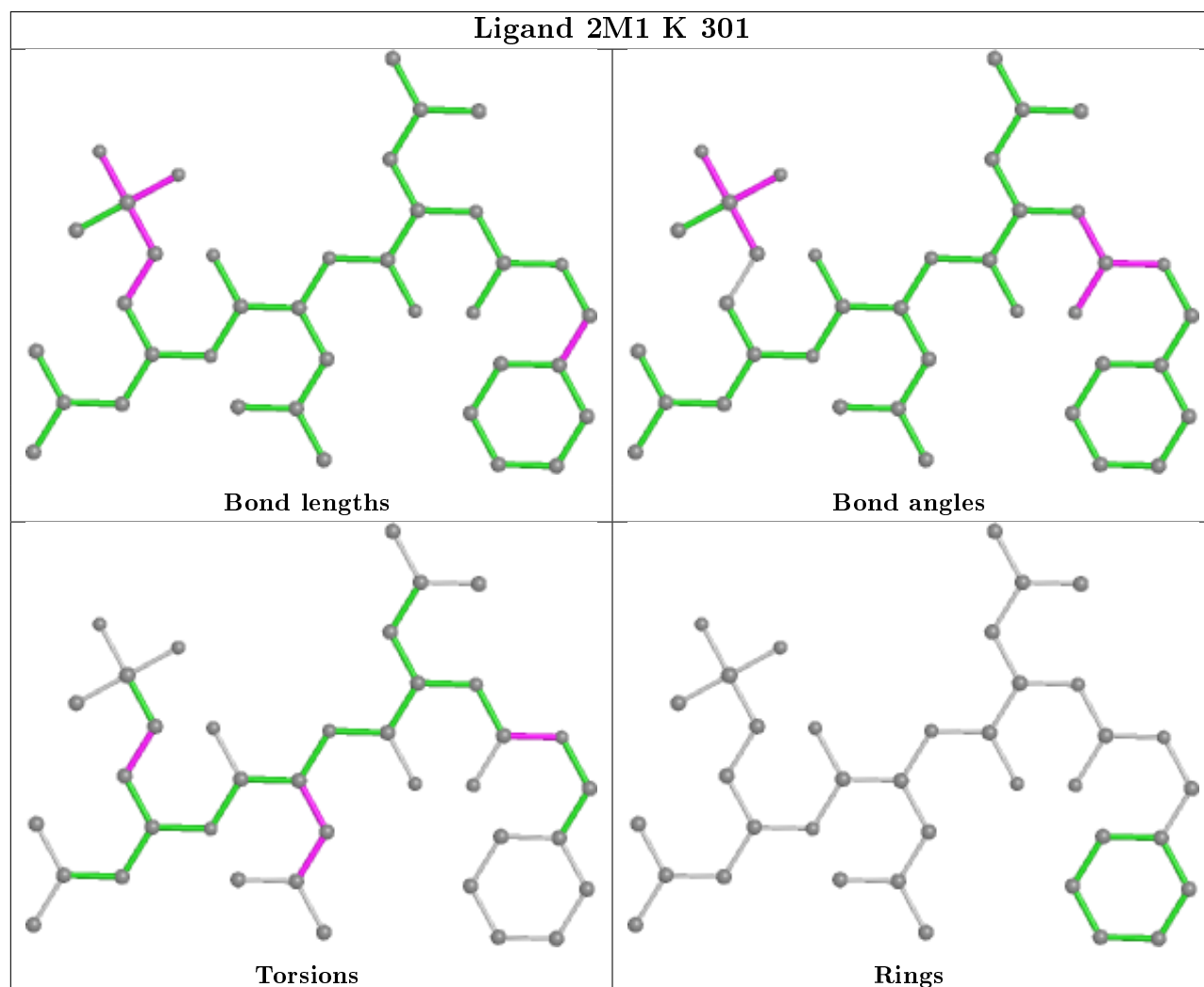
Mol	Chain	Res	Type	Atoms
16	Y	301	2M1	O8-C7-O6-C5
16	Y	301	2M1	N9-C7-O6-C5
16	K	301	2M1	O8-C7-O6-C5
16	K	301	2M1	N9-C7-O6-C5
16	K	301	2M1	N16-C17-C18-C19
16	Y	301	2M1	N16-C17-C18-C19
16	K	301	2M1	C22-C17-C18-C19
16	Y	301	2M1	C22-C17-C18-C19
16	K	301	2M1	S42-C26-C41-C25
16	Y	301	2M1	S42-C26-C41-C25
16	K	301	2M1	C17-C18-C19-C20

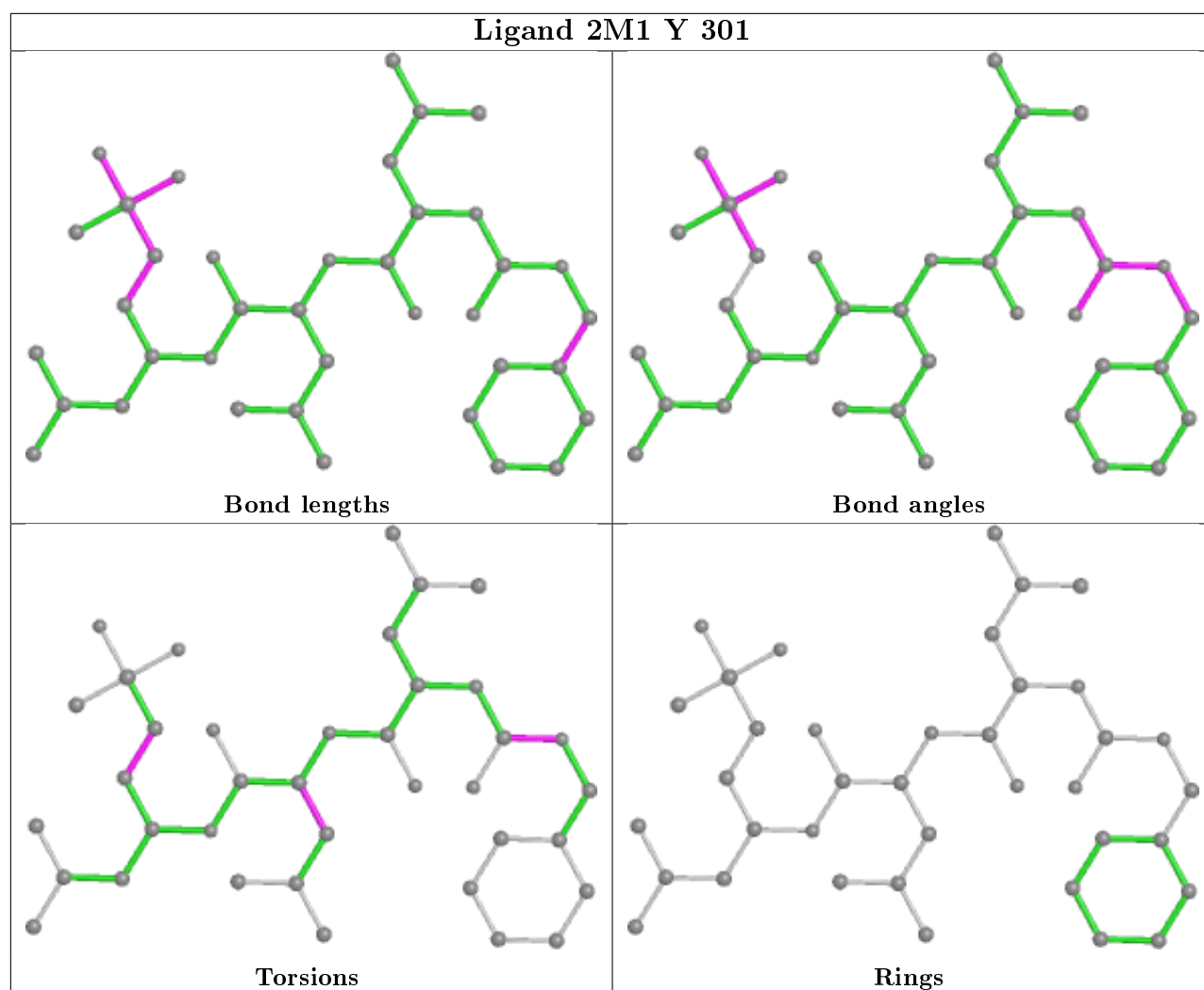
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.70	1 (0%) 92 79	34, 54, 89, 118	0
1	O	250/250 (100%)	-0.68	1 (0%) 92 79	38, 59, 93, 121	0
2	B	244/258 (94%)	-0.61	4 (1%) 72 44	34, 59, 100, 154	0
2	P	244/258 (94%)	-0.57	7 (2%) 51 23	41, 59, 107, 156	0
3	C	240/254 (94%)	-0.57	4 (1%) 70 41	38, 60, 112, 142	0
3	Q	240/254 (94%)	-0.47	8 (3%) 46 20	38, 69, 123, 149	0
4	D	235/260 (90%)	-0.69	1 (0%) 92 79	35, 60, 87, 108	0
4	R	235/260 (90%)	-0.60	1 (0%) 92 79	38, 65, 100, 117	0
5	E	231/234 (98%)	-0.64	1 (0%) 92 79	37, 65, 94, 130	0
5	S	231/234 (98%)	-0.62	1 (0%) 92 79	41, 67, 99, 128	0
6	F	243/288 (84%)	-0.68	3 (1%) 79 54	38, 59, 101, 134	0
6	T	243/288 (84%)	-0.69	0 100 100	40, 58, 96, 115	0
7	G	241/252 (95%)	-0.73	0 100 100	34, 54, 84, 140	0
7	U	241/252 (95%)	-0.73	1 (0%) 92 79	36, 54, 87, 127	0
8	H	222/232 (95%)	-0.78	2 (0%) 84 63	31, 50, 70, 130	0
8	V	222/232 (95%)	-0.77	2 (0%) 84 63	35, 53, 74, 130	0
9	I	204/205 (99%)	-0.90	1 (0%) 91 75	33, 51, 74, 101	0
9	W	204/205 (99%)	-0.89	1 (0%) 91 75	35, 51, 76, 97	0
10	J	195/198 (98%)	-0.82	0 100 100	33, 49, 80, 119	0
10	X	195/198 (98%)	-0.84	1 (0%) 91 75	34, 51, 74, 135	0
11	K	212/212 (100%)	-0.83	0 100 100	31, 50, 74, 87	0
11	Y	212/212 (100%)	-0.83	0 100 100	32, 54, 80, 99	0
12	L	222/222 (100%)	-0.87	0 100 100	30, 53, 73, 95	0
12	Z	222/222 (100%)	-0.84	0 100 100	30, 53, 76, 93	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.82	0 100 100	34, 52, 71, 82	0
13	a	233/246 (94%)	-0.85	0 100 100	31, 49, 69, 80	0
14	N	196/196 (100%)	-0.88	0 100 100	31, 47, 70, 94	0
14	b	196/196 (100%)	-0.86	1 (0%) 91 75	34, 48, 71, 98	0
All	All	6336/6614 (95%)	-0.73	41 (0%) 89 72	30, 55, 92, 156	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	219	ALA	5.6
8	V	222	ASP	5.2
2	P	220	ASN	4.9
2	B	219	ALA	4.7
2	B	218	GLY	4.4
2	B	220	ASN	4.1
5	S	202	ASP	3.8
8	H	222	ASP	3.6
9	I	1	SER	3.3
2	B	221	ASP	3.3
2	P	218	GLY	3.2
2	P	221	ASP	3.2
8	V	221	CYS	3.1
1	A	2	THR	3.1
7	U	242	GLN	2.9
3	Q	239	GLN	2.8
3	C	206	LYS	2.8
3	Q	240	GLU	2.8
3	Q	236	GLN	2.6
2	P	222	GLY	2.6
2	P	59	ASP	2.5
3	Q	206	LYS	2.4
3	C	240	GLU	2.4
5	E	202	ASP	2.4
8	H	221	CYS	2.4
9	W	1	SER	2.3
3	Q	203	THR	2.3
6	F	202	ASP	2.2
4	R	241	ALA	2.2
3	Q	49	THR	2.2
1	O	249	ALA	2.2
3	Q	237	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	P	51	VAL	2.2
3	Q	238	LYS	2.1
4	D	242	GLU	2.1
3	C	239	GLN	2.1
6	F	2	THR	2.1
6	F	244	ASN	2.1
3	C	49	THR	2.0
14	b	105	LYS	2.0
10	X	194	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

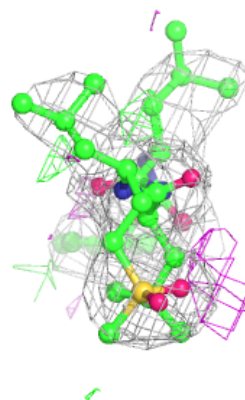
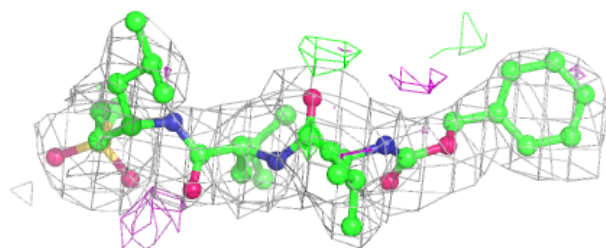
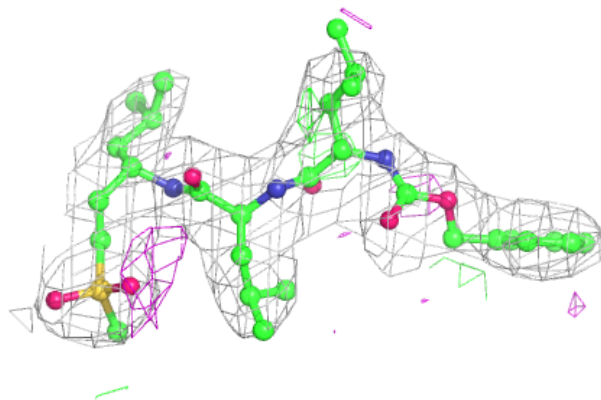
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

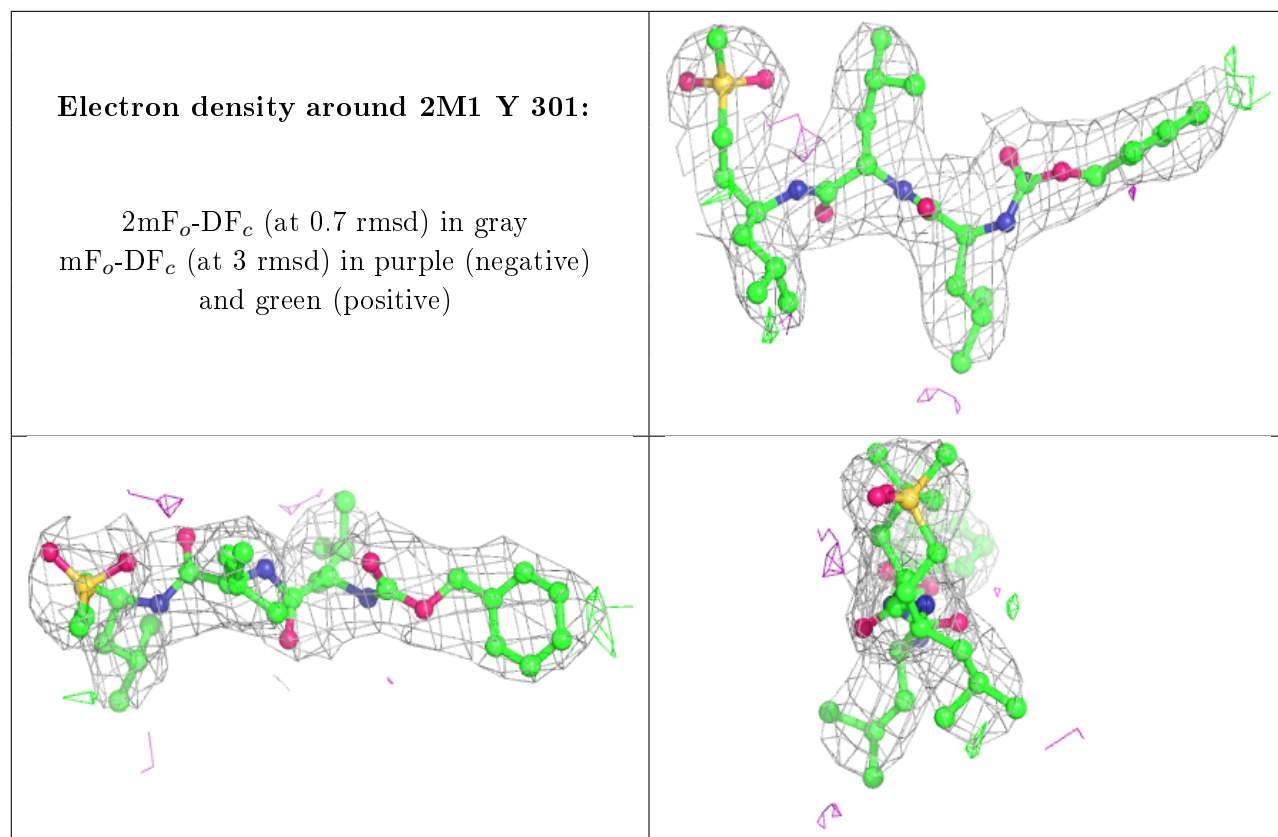
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	2M1	K	301	38/38	0.93	0.20	54,64,80,81	0
15	MG	H	301	1/1	0.94	0.13	38,38,38,38	0
16	2M1	Y	301	38/38	0.95	0.19	55,65,78,80	0
15	MG	K	302	1/1	0.95	0.10	53,53,53,53	0
15	MG	Z	301	1/1	0.96	0.21	54,54,54,54	0
15	MG	G	301	1/1	0.97	0.08	64,64,64,64	0
15	MG	I	301	1/1	0.97	0.10	45,45,45,45	0
15	MG	N	201	1/1	0.97	0.13	43,43,43,43	0
15	MG	V	301	1/1	0.98	0.06	59,59,59,59	0
15	MG	Y	302	1/1	0.99	0.05	42,42,42,42	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 2M1 K 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.